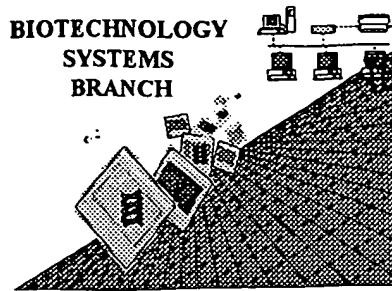


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JUN 07 2001

BIOTECHNOLOGY
SYSTEMS
BRANCH



TECH CENTER 1600/2900

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/734,239A
Source: 1600
Date Processed by STIC: 5/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/734,237A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) 2 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/734,237A

DATE: 05/21/2001
TIME: 11:42:24

Input Set : A:\B583_40608.txt
Output Set: N:\CRF3\05212001\I734237A.raw

Does Not Comply
Corrected Diskette Needed

pp 1,3,6

01/2

```

3 <110> APPLICANT: Rozzell, J. David
4   Bui, Peter
5   Hua, Ling
7 <120> TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
9 <130> FILE REFERENCE: B583:40608
11 <140> CURRENT APPLICATION NUMBER: US/09/734,237A
11 <141> CURRENT FILING DATE: 2000-12-08
11 <150> PRIOR APPLICATION NUMBER: 09/494,921
12 <151> PRIOR FILING DATE: 2000-01-31
14 <160> NUMBER OF SEQ ID NOS: 79
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1197
20 <212> TYPE: DNA
21 <213> ORGANISM: Pseudomonas putida
23 <400> SEQUENCE: 1
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26 ccccaggacc acggcggcgc actggtgcca cgggtctacc agaccgcgac gttcaccttc      120
28 cccaccgtgg aatacggcgc tgcgtgcttt gccggcgagc aggcggggca tttctacagc      180
30 cgcattctcca accccaccct caacctgctg gaagcacgca tggcctcgct ggaaggcggc      240
32 gaggcggggc tggcgctggc ctcgggcatg ggggcatga cgtccacgct atggacactg      300
34 ctgcgccacg gtcacgaggt gctgctgggc aacaccctgt acggctgcac ctttgccttc      360
36 ctgcaccacg gcatcggcga gttcggggtc aagctgcgcc atgtggacat ggccgacctg      420
38 caggcactgg aggcggccat gacgcgggcc acccggtgta tctatttcga gtcgcgggcc      480
40 aaccccaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcacg caagcacggc      540
42 gcgaccgtgg tggctcgacaa cacctactgc acgccgtacc tgcaacggcc actggagctg      600
44 ggcgcgcgacc tgggtggtgca ttcggccacc aagtacctga gcggccatgg cgacatcact      660
46 gctggcattg tgggtgggcag ccaggcactg gtggaccgta tacgtctgca gggcctcaag      720
48 gacatgaccg gtgcggtgct ctgcgcccat gacgccgcac tgttgatgcg cggcatcaag      780
50 accctcaacc tgcgcattga ccgccactgc gccaacgctc aggtgctggc cgagttcctc      840
52 gcccggcagc cgcagggtga gctgatccat taccggggcc tggcgagctt cccgcagtac      900
54 accctggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc      960
56 ggcacatcgt cggggcggcg gttcatgaac gccctgcaac tgttcagccg cgcggtgagc     1020
58 ctgggcatg cgcagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc     1080
60 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcggttgtc ggtggggctg     1140
62 gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgcctga      1197
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 399
67 <212> TYPE: PRT
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <221> NAME/KEY: misc_feature
72 <223> OTHER INFORMATION: Glycine residue inserted at position 2
75 <400> SEQUENCE: 2
77 Met Gly His Gly Ser Asn Lys Leu Pro Gly Phe Ala Thr Arg Ala Ile
78 1           5           10           15
80 His His Gly Tyr Asp Pro Gln Asp His Gly Gly Ala Leu Val Pro Pro

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see item 12 on Enr Summary Sheet

RAW SEQUENCE LISTING DATE: 05/21/2001
 PATENT APPLICATION: US/09/734,237A TIME: 11:42:24

Input Set : A:\B583_40608.txt
 Output Set: N:\CRF3\05212001\I734237A.raw

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81          20          25          30
83 Val Tyr Gln Thr Ala Thr Phe Thr Pro Thr Val Glu Tyr Gly Ala
84          35          40          45
86 Ala Cys Phe Ala Gly Glu Gln Ala Gly His Pro Tyr Ser Arg Ile Ser
87          50          55          60
89 Asn Pro Thr Leu Asn Leu Leu Gln Ala Arg Met Ala Ser Leu Glu Gly
90 65          70          75          80
92 Gly Glu Ala Gly Leu Ala Leu Ala Ser Gly Met Gly Ala Ile Thr Ser
93          85          90          95
95 Thr Leu Tyr Thr Leu Leu Arg Pro Gly Asp Glu Val Leu Leu Gly Asn
96          100          105          110
98 Thr Leu Tyr Gly Cys Thr Phe Ala Phe Leu His His Gly Ile Gly Glu
99          115          120          125
101 Phe Gly Val Lys Leu Arg His Val Asp Met Ala Asp Leu Gln Ala Leu
102          130          135          140
104 Glu Ala Ala Met Thr Pro Ala Thr Arg Val Ile Tyr Phe Glu Ser Pro
105 145          150          155          160
107 Ala Asn Pro Asn Met His Met Ala Asp Ile Ala Gly Val Ala Lys Ile
108          165          170          175
110 Ala Arg Lys His Gly Ala Thr Val Val Val Asp Asn Thr Tyr Cys Thr
111          180          185          190
113 Pro Tyr Leu Gln Arg Pro Leu Gln Leu Gly Ala Asp Leu Val Val His
114          195          200          205
116 Ser Ala Thr Lys Tyr Leu Ser Gly His Gly Asp Ile Thr Ala Gly Ile
117          210          215          220
119 Val Val Gly Ser Gln Ala Leu Val Asp Arg Ile Arg Leu Gln Gly Leu
120 225          230          235          240
122 Lys Asp Met Thr Gly Ala Val Leu Ser Pro His Asp Ala Ala Leu Leu
123          245          250          255
125 Met Arg Gly Ile Lys Thr Leu Asn Leu Arg Met Asp Arg His Cys Ala
126          260          265          270
128 Asn Ala Gln Val Leu Ala Glu Phe Leu Ala Arg Gln Pro Gln Val Glu
129          275          280          285
131 Leu Ile His Tyr Pro Gly Leu Ala Ser Phe Pro Gln Tyr Thr Leu Ala
132          290          295          300
134 Arg Gln Gln Met Ser Gln Pro Gly Gly Met Ile Ala Phe Glu Leu Lys
135 305          310          315          320
137 Gly Gly Ile Gly Ala Gly Arg Arg Phe Met Asn Ala Leu Gln Leu Phe
138          325          330          335
140 Ser Arg Ala Val Ser Leu Gly Asp Ala Glu Ser Leu Ala Gln His Pro
141          340          345          350
143 Ala Ser Met Thr His Ser Ser Tyr Thr Pro Glu Glu Arg Ala His Tyr
144          355          360          365
146 Gly Ile Ser Glu Gly Leu Val Arg Leu Ser Val Gly Leu Glu Asp Ile
147          370          375          380
149 Asp Asp Leu Leu Ala Asp Val Gln Gln Ala Leu Lys Ala Ser Ala
150 385          390          395
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 1202

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RAW SEQUENCE LISTING DATE: 05/21/2001
 PATENT APPLICATION: US/09/734,237A TIME: 11:42:24

Input Set : A:\B583_40608.txt
 Output Set: N:\CRF3\05212001\I734237A.raw

```

154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial sequence
157 <220> FEATURE:
158 <221> NAME/KEY: misc_feature
159 <223> OTHER INFORMATION: Sequence derived from Pseudomonas putida methionine gamma-lyase;
160     glycine codon inserted to incorporate restriction site, and numero restriction
161     us naturally occurring codons replace replace what?
164 <400> SEQUENCE: 3
165 catgggtcac ggctccaaca aactgccggg ctttctacc cgcgctatcc accacggtta      60
166 tgacccgcag gatcacggtg gtgcactggt tccgccggtt taccagactg ctactttcac      120
167 cttcccgacc gttgaatacg gcgctgcgtg ctttctggc gaacaggctg gtcacttcta      180
168 ctcccgtatc tccaaccoga ccctgaacct gctggaagca cgtatggcat ctctggaagg      240
169 cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta ccctgtggac      300
170 cctgctgcgt ccgggtgacg aagttctgct gggcaacacc ctgtatggtt gtacttttgc      360
171 ttctctgcac cacggtatcg gtgaattcgg cgttaaactg cgtcacgtag atatggctga      420
172 cctgcaggca ctggaagcgg ctatgacccc ggctaccggt gttatctact tcgaatcccc      480
173 ggctaaccgg aacatgcaca tggctgacat cgcagggtgt gctaaaatcg ctctgaagca      540
174 cggcgctacc gtagttgttg ataacaccta ctgtactccg tacctgcaac gtccgctgga      600
175 actgggcgct gacctggttg ttacttcgcg tactaaatac ctgtccggcc acggcgacat      660
176 cactgctggc atcgtagtag gctcccaggc actggttgac cgtatccgtc tgcaaggctc      720
177 gaaagacatg accggcgctg ttctgtcccc gcacgacgca gcaactgctg tgcgtggtat      780
178 caagaccctg aacctgcgta tggaccgtca ctgtgctaac gctcaggtag tggctgaatt      840
179 cctggctcgt cagccgcagg tagaactgat ccactatccg ggctggctt cctcccgca      900
180 gtacactctg gcacgtcagc agatgtccca gccgggcggg atgatcgctt tcgaactgaa      960
181 ggggtggcatc ggcgctggtc gtcgtttcat gaacgctctg cagctgttct cccgtgcggt      1020
182 ttccctgggt gacgctgaat ccctggcgca gcacccggca tccatgactc actcctccta      1080
183 cactccggaa gaacgtgcgc actacggcat ctccgaaggc ctggttcgtc tgtctgttgg      1140
184 tctggaagac atcgatgatc tgctggcaga cgttcagcag gctctgaagg ctacgccttg      1200
205 ag
208 <210> SEQ ID NO: 4
209 <211> LENGTH: 426
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial sequence
213 <220> FEATURE:
214 <221> NAME/KEY: misc_feature
215 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
218 <400> SEQUENCE: 4
219 catgggtcac ggctccaaca aactgccggg ctttctacc cgcgctatcc accacggtta      60
220 tgacccgcag gatcacggtg gtgcactggt tccgccggtt taccagactg ctactttcac      120
221 cttcccgacc gttgaatacg gcgctgcgtg ctttctggc gaacaggctg gtcacttcta      180
222 ctcccgtatc tccaaccoga ccctgaacct gctggaagca cgtatggcat ctctggaagg      240
223 cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta ccctgtggac      300
224 cctgctgcgt ccgggtgacg aagttctgct gggcaacacc ctgtatggtt gtacttttgc      360
225 ttctctgcac cacggtatcg gtgaattcgg cgttaaactg cgtcacgtag atatggctga      420
233 cctgca
236 <210> SEQ ID NO: 5
237 <211> LENGTH: 441
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial sequence

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RAW SEQUENCE LISTING DATE: 05/21/2001
 PATENT APPLICATION: US/09/734,237A TIME: 11:42:24

Input Set : A:\B583_40608.txt
 Output Set: N:\CRF3\05212001\I734237A.raw

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241 <220> FEATURE:
242 <221> NAME/KEY: misc_feature
243 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
246 <400> SEQUENCE: 5
247 caagaggcca tgggtcacgg ctccaacaaa ctgccgggct ttgctaccgg cgctatccac      60
249 cacgggttatg acccgagga tcacgggtgg gcactgggtc cgccgggtta ccagactgct      120
251 actttcacct tcccgaccgt tgaatacggc gctgcgtgct ttgctggcga acaggctggg      180
253 cactttctact cccgtatctc caaccggacc ctgaacctgc tggagcacg tatggcatct      240
255 ctggaaggcg gcgaagctgg tctggcgctg gcactctggt tgggcgcgat cactctacc      300
257 ctgtggagccc tgctgcgtcc gggtagcgaa gttctgctgg gcaacaccct gtatggttgt      360
259 acttttgctt tctgcacca cggtatcggg gaattcggcg ttaaactgcg tcacgtagat      420
261 atggctgacc tgcaggcact g                                     441
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 410
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial sequence
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
274 <400> SEQUENCE: 6
275 ggcactggaa gcggctatga ccccggttac ccgtgttatc tacttcgaat ccccggttaa      60
277 cccgaacatg cacatggctg acatcgaggg tggtgctaaa atcgctcgta agcacggcgc      120
279 taccgtagtt gttgataaca cctactgtac tccgtacctg caacgtccgc tggaaactggg      180
281 cgctgacctg gttgttcaact ccgtactaa atacctgtcc ggccacggcg acatcactgc      240
283 tggcatcgta gtaggtccc aggcactggg tgaccgtatc cgtctgcaag gtctgaaaga      300
285 catgaccggc gctgttctgt cccgcacga cgcagcactg ctgatgcgtg gtatcaagac      360
287 cctgaacctg cgtatggacc gtcactgtgc taacgctcag gtactggctg      410
290 <210> SEQ ID NO: 7
291 <211> LENGTH: 430
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial sequence
295 <220> FEATURE:
296 <221> NAME/KEY: misc_feature
297 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
300 <400> SEQUENCE: 7
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303 tccccggcta acccgaacat gcacatggct gacatcgag gtgttgctaa aatcgctcgt      120
305 aagcacggcg ctaccgtagt tgttgataac acctactgta ctccgtacct gcaacgtccg      180
307 ctggaactgg gcgctgacct ggtgttcac tccgctacta aatacctgtc cggccacggc      240
309 gacatcactg ctggcatcgt agtaggtccc caggcactgg ttgaccgtat ccgtctgcaa      300
311 ggtctgaaag acatgaccgg cgctgttctg tccccgcag acgcagcact gctgatgcgt      360
313 ggtatcaaga cctgaacct gcgtatggac cgctactgtg ctaacgctca ggtactggct      420
315 gaattcctgg                                     430
318 <210> SEQ ID NO: 8
319 <211> LENGTH: 366
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial sequence
323 <220> FEATURE:
324 <221> NAME/KEY: misc_feature

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RAW SEQUENCE LISTING DATE: 05/21/2001
 PATENT APPLICATION: US/09/734,237A TIME: 11:42:24

Input Set : A:\B583_40608.txt
 Output Set: N:\CRF3\05212001\I734237A.raw

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325 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
328 <400> SEQUENCE: 8
329 aattcctggc tcgtcagccg caggtagaac tgatccacta tccgggcttg gcttccttcc      60
331 cgcagtacac tctggcacgt cagcagatgt cccagccggg cggtatgacg gctttcgaac      120
333 tgaagggtgg catcgccgct ggctcgtcgt tcatgaacgc tctgcagctg ttctcccgtg      180
335 cggtttccct ggggtgacgt gaatccctgg cgcagcaccg gccatccatg actcactcct      240
337 cctacactcc ggaagaacgt gcgcactacg gcactctccg aggcctgggt cgtctgtctg      300
339 ttgggtctga agacatcgat gatctgctgg cagacgttca gcaggctctg aaggctagcg      360
341 cttgag                                         366
344 <210> SEQ ID NO: 9
345 <211> LENGTH: 383
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial sequence
349 <220> FEATURE:
350 <221> NAME/KEY: misc_feature
351 <223> OTHER INFORMATION: Cloning fragment of SEQ ID NO. 3
354 <400> SEQUENCE: 9
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359 ttctgaactg aagggtggca tcggcgctgg tcgtcgtttc atgaacgctc tgcagctgtt      180
361 ctcccgtgcg gtttccctgg gtgacgtgta atccctggcg cagcaccgg catccatgac      240
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367 ggctagcgct tgaggatcca cca                                         383
370 <210> SEQ ID NO: 10
371 <211> LENGTH: 33
372 <212> TYPE: DNA
373 <213> ORGANISM: Artificial Sequence
375 <220> FEATURE:
376 <221> NAME/KEY: misc_feature
377 <223> OTHER INFORMATION: Primer/template derived from SEQ ID NO. 3
380 <400> SEQUENCE: 10
381 caagaggcca tgggtcacgg ctccaacaaa ctg                                         33
384 <210> SEQ ID NO: 11
385 <211> LENGTH: 114
386 <212> TYPE: DNA
387 <213> ORGANISM: Artificial Sequence
389 <220> FEATURE:
390 <221> NAME/KEY: misc_feature
391 <223> OTHER INFORMATION: Primer/template derived from SEQ ID NO. 3
394 <400> SEQUENCE: 11
395 cagggtcca acaaaactgcc gggctttgct acccgcgcta tccaccacgg ttatgaccgg      60
397 caggatcacg gtggtgcact ggtccgcgg gtttaccaga ctgctacttt cacc          114
400 <210> SEQ ID NO: 12
401 <211> LENGTH: 116
402 <212> TYPE: DNA
403 <213> ORGANISM: Artificial Sequence
405 <220> FEATURE:
406 <221> NAME/KEY: misc_feature

```

<210> 55
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>

<221> misc_feature

<223> Synthetic gene derived from Sus scrofa L-aromatic amino acid decarboxylase, having numerous codons replaced with others encoding the same amino acids to reduce the free energy of folding, and a glycine inserted after the initiating methionine codon to insert a restriction site

<400> 55

↑
insert "e"

Per 1.823

of
sequence

Rules,
4 lines

maximum

for <223>
response

Please ensure
all <223> responses
are 4 lines maximum

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/734,237A

DATE: 05/21/2001

TIME: 11:42:25

Input Set : A:\B583_40608.txt

Output Set: N:\CRF3\05212001\I734237A.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2261 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2555 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2848 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3197 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3705 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:4104 M:259 W: Allowed number of lines exceeded, <223> Other Information: